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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/715,249DATE: 12/06/2000
TIME: 14:51:42Input Set : A:\31192 Seq. Listing.txt
Output Set: N:\CRF3\12062000\I715249.raw

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3 <110> APPLICANT: NOVARTIS AG
4   VERES, GABOR
5   PIPPIG, SUSANNE
7 <120> TITLE OF INVENTION: selectable cell surface marker genes
9 <130> FILE REFERENCE: 4-31192
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/715,249
C--> 11 <141> CURRENT FILING DATE: 2000-11-17
11 <150> PRIOR APPLICATION NUMBER: us 60/166594
12 <151> PRIOR FILING DATE: 1999-11-19
14 <150> PRIOR APPLICATION NUMBER: us 09/539248
15 <151> PRIOR FILING DATE: 2000-03-30
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: PatentIn version 3.0
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22 <211> LENGTH: 3633
23 <212> TYPE: DNA
24 <213> ORGANISM: EGFR
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31 tggggcactt ttgagatca ttttctcagc ctccagaaggc tgttcaataa ctgtgaggtg   180
33 gtccttgqga atttggaaat tacctatgtg cagaggaatt atgatcttct cttctttaaag   240
35 accatccagg aggtggctgg ttatgtcctc attgccctca accaagtggc qcgaaatcct   300
37 tlygaaaacc tgcagatcat cagaggaagt atgtactacg aaatctcta tgccttagca   360
39 gtcttaacta actatgatgc aaataaaacc ggaactgaagg agctgcccat gagaaatta   420
41 caggaaatcc tgcattggcg cgtgcgggttc agcaacaaacc ctgcctctgtg caacttggag   480
43 agcatccagt ggcgggacat agtcagcagt gaactttctc gcaacatgtc gatggacttc   540
45 cagaaccacc tgggcagctg ccaaaagtgt gatccaagct gtcaccaatg gagctgtctg   600
47 ggtgcaggag aggagaaact ccagaaactg accaaaatca tctgtgccca gcagtgctcc   660
49 gggcgctgcc gtgcgaagtc cccagtgac tgcctgccca accaagtgtg tgcaggctgc   720
51 acaggccccc gggagagcga ctgcttggtc tgcgcgaatc tccagagaga agccacgtgc   780
53 aaggacacct gcccaccact catgtctcac aaccccacca cgtaccagat ggaatgtgaac   840
55 cccgagggca aatlacagct ttgtgccacc tgcgtgaaga agtgccccg taattatgtg   900
57 gtgacagatc acggtctcgt cgtccgaacc tgtggggccg acaactatga gatggagaa   960
59 gacggcgtcc gcaagtgtaa gaagtgcgaa gggccttgcc gcaaaagtgt taacgggaata   1020
61 ggtatgtgtg aatltaaaga ctcactctcc ataaatgcta cgaalattaa acacttcaaa   1080
63 aactgcacct ccatcagttg cgaatctcac atcctgcctg tggcalttag ggtgactcc   1140
65 ttacacata ctccctctcl ggaaccacag gaactggata ttctgaaaac cgtaaaggaa   1200
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69 gagaacctag aatcatatcg cggcaggacc aagcaacatg gtcaglttct tcttgagtc   1320
71 gtcagcctga acataacatc ctgggatta cgtccctca agagataaag tgaaggagat   1380
73 gtgataatll caggaaacaa aaatttgtgc tatgcaata caataaactg gaaaaaactg   1440
75 ttggaacct ccgctcagaa aacraaantt ataagcaaca gaqgtqaaaa cagctgcag   1500
77 gccacagccc aggtctgca tgccttgctc tccccgagg gctgctgggg cccggagccc   1560
79 aqggactacg tctcttgccc gaatgtcagc cagggcaggg aatgcgttga caagtgcag   1620
81 ctctctgggg gtgagccagg ggaatttgg gagaaactct agtgcataca gtgccacca   1680
83 gagtgcctgc ctacggccat gaacatcacc tgcacaggac ggggaccaga caactgtatc   1740

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85 cagtggtgcc actacattga cggccccac tgggtcaaga cctgccgggc aggaatcatg 1800
87 ggagaaaaac acaccccggt clggaagtac gcagacgccc gccatgltgt ccacctgtgc 1860
89 catccaaact qcacctacgg atgcactggg ccaqgtcttg aaggtcttcc aacgaatggg 1920
91 cetaagatcc cgtcatcgc cactgggatg gtggggggcc tctctttgct gctggtggtg 1980
93 gccctgggga tgggcccctt calgcgaagc cggccacatc ttcggaagcg cagctgtcgg 2040
95 aggtctgtgc aggaagggga gcltgtggag cclcttacac ccagtggaga agctcccaac 2100
97 caaactctct tgaqgattct gaagqaaact gaattcaaaa agatcaaaat gctgggctcc 2160
99 ggtgcattcg gcaagggtga taagggaact tggatcccaq aaggtgagaa agtkaaaatt 2220
101 cccgtcgcta tcaaggaaat aaggaagca acatctccga aagccaacaa ggaatccctc 2280
103 gatgaagcct acgtgatggc cagcgtggac aacccccacg tgtgccctct gctgggcata 2340
105 tgcctacact ccacgttgcg actcactacg cagctcatgc ccttcggtct cctccctggc 2400
107 tatgtccggg aacacaaaga caatattgac tcccaqtacc tgcctcaact gtgtgtgtca 2460
109 atcgcaaaag qcatgaacta cttggaggac cgtcgtcttg tgcacgcgca cctggcagcc 2520
111 aggaacgtac tgggtgaaac accgcagcat qtcaaatcca caqatttttg gcltggcгаа 2580
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117 ggggtgacgg ttggggagtl gatgaccttl ggaaccagac catatgacgg aatccctgcc 2760
119 agcgagatct cctccactct ggaagaaagg gaacgcctcc clcagccacc catatgtacc 2820
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123 ttccttgact tgatcatcga attctcraaa atggcccgag acccccagcg ctaccttgtc 2940
125 attcaagggg atgaagaat qcatlttgca agtctctacg actccaactt ctacctgtcc 3000
127 ctgatggatg aagaagacat ggaagacgtg gtggatgccc acgagtacct catccacag 3060
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131 accagcaaca attccacgtl ggtlgtcatt galagaaatg gactgcaaaq ctgtcccatc 3180
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135 aqcatagagc acaccttctt cccagtgcct gaatacataa accagtcctt tcccaaaagg 3300
137 ccgctgtgct ctgttcagaa tcttctctat cacaatcagc ctctgaaccc cgcgcrcagc 3360
139 agagacccac actaccagga ccccccagc actgcagtgg gcaaccocga gtatctcaac 3420
141 actgtccagc ccacctgtgt caacagcaca ttcgacagcc ctcccactg ggcacagaaa 3480
143 ggcagccacc aatttagctt ggaacaacct gactaccagc aggaattctt tcccaaggaa 3540
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150 <210> SEQ ID NO: 2
151 <211> LENGTH: 1210
152 <212> TYPE: PRI
153 <213> ORGANISM: EGFR
155 <400> SEQUENCE: 2
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158 1 5 10 15
160 Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
161 20 25 30
163 Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
164 35 40 45
166 Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
167 50 55 60
169 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
170 65 70 75 80
172 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
173 85 90 95

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175 Glu Arg Ile Pro Leu Glu Asn Leu Glu Ile Ile Arg Gly Asn Met Tyr
176           100           105           110
178 Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
179           115           120           125
181 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
182           130           135           140
184 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
185           145           150           155           160
187 Ser Ile Glu Lys Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
188           165           170           175
190 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
191           180           185           190
193 Ser Cys Pro Asn Gly Ser Cys Lys Gly Ala Gly Glu Glu Asn Cys Glu
194           195           200           205
196 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
197           210           215           220
199 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
200           225           230           235           240
202 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
203           245           250           255
205 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
206           260           265           270
208 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
209           275           280           285
211 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
212           290           295           300
214 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
215           305           310           315           320
217 Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
218           325           330           335
220 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
221           340           345           350
223 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
224           355           360           365
226 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
227           370           375           380
229 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
230           385           390           395           400
232 Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
233           405           410           415
235 Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
236           420           425           430
238 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
239           435           440           445
241 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
242           450           455           460
244 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
245           465           470           475           480
247 Phe Gly Thr Ser Gly Glu Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu

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248		485		490		195
250	Asn Ser Cys	Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro				
251		500		505		510
253	Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn					
254		515		520		525
256	Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly					
257		530		535		540
259	Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro					
260	545		550		555	560
262	Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro					
263		565		570		575
265	Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val					
266		580		585		590
268	Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp					
269		595		600		605
271	Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys					
272		610		615		620
274	Ihr Tyr Gly Cys Ihr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly					
275	625		630		635	640
277	Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu					
278		645		650		655
280	Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His					
281		660		665		670
283	Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu					
284		675		680		685
286	Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Glu Ala Leu Leu					
287		690		695		700
289	Arg Ile Leu Lys Glu Thr Gln Phe Lys Lys Ile Lys Val Leu Gly Ser					
290	705		710		715	720
292	Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu					
293		725		730		735
295	Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser					
296		740		745		750
298	Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser					
299		755		760		765
301	Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser					
302		770		775		780
304	Ihr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp					
305	785		790		795	800
307	Iyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn					
308		805		810		815
310	Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg					
311		820		825		830
313	Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro					
314		835		840		845
316	Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala					
317		850		855		860
319	Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp					
320	865		870		875	880

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322 Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
323      885      890      895
325 Val Irp Ser Tyr Gly Val Thr Val Irp Glu Leu Met Thr Phe Gly Ser
326      900      905      910
328 Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
329      915      920      925
331 Lys Glu Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Iyr
332      930      935      940
334 Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
335 945      950      955      960
337 Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
338      965      970      975
340 Arg Iyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
341      980      985      990
343 Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
344      995      1000      1005
346 Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
347      1010      1015      1020
349 Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
350      1025      1030      1035
352 Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
353      1040      1045      1050
355 Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
356      1055      1060      1065
358 Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
359      1070      1075      1080
361 Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
362      1085      1090      1095
364 Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
365      1100      1105      1110
367 Pro Leu Asu Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
368      1115      1120      1125
370 His Ser Thr Ala Val Gly Asn Pro Gln Tyr Leu Asn Thr Val Gln
371      1130      1135      1140
373 Pro Thr Cys Val Asn Ser Iyr Phe Asp Ser Pro Ala His Trp Ala
374      1145      1150      1155
376 Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
377      1160      1165      1170
379 Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
380      1175      1180      1185
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383      1190      1195      1200
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386      1205      1210
388 <210> SEQ ID NO: 3
389 <211> LENGTH: 31
390 <212> TYPE: DNA
391 <213> ORGANISM: primer
393 <400> SEQUENCE: 3

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VERIFICATION SUMMARY DATE: 12/06/2000
PATENT APPLICATION: US/09/715,249 TIME: 14:51:43

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date